

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/020,478

DATE: 01/02/2002
TIME: 11:19:18

Input Set : A:\RTS-0303 Sequence Listing.txt
Output Set: N:\CRF3\01022002\J020478.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: C. Frank Bennett
4 Kenneth Dobie
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF B-CELL ASSOCIATED PROTEIN EXPRESSION
8 <130> FILE REFERENCE: RTS-0303
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/020,478
C--> 10 <141> CURRENT FILING DATE: 2001-12-13
10 <160> NUMBER OF SEQ ID NOS: 88
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense Oligonucleotide
22 <400> SEQUENCE: 1 20
23 tccgtcatcg ctcctcaggg
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2 20
36 atgcattctg cccccaagga
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 1416
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
44 <220> FEATURE:
46 <220> FEATURE: *delete*
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (186)...(1085)
50 <400> SEQUENCE: 3
51 aagttcgggt ccgtagtggg ctaaggggga gggtttcaaa gggagcgcac ttccgctgcc 60
53 ctttcttttcg ccagccttac gggcccgaac cctcgtgtga aggggtgcagt acctaagccg 120
55 gagcggggta gaggcgggcc ggcacccctc tctgacctcc agtgccgccg gcctcaagat 180
57 cagac atg gcc cag aac ttg aag gac ttg gcg gga cgg ctg ccc gcc ggg 230
58 Met Ala Gln Asn Leu Lys Asp Leu Ala Gly Arg Leu Pro Ala Gly 15
59 1 5 10 15
61 ccc cgg ggc atg ggc acg gcc ctg aag ctg ttg ctg ggg gcc ggc gcc 278
62 Pro Arg Gly Met Gly Thr Ala Leu Lys Leu Leu Leu Gly Ala Gly Ala 30
63 20 25 30
65 gtg gcc tac ggt gtg cgc gaa tct gtg ttc acc gtg gaa ggc ggg cac 326
66 Val Ala Tyr Gly Val Arg Glu Ser Val Phe Thr Val Glu Gly Gly His 45
67 35 40 45
69 aga gcc atc ttc ttc aat cgg atc ggt gga gtg cag cag gac act atc 374
70 Arg Ala Ile Phe Phe Asn Arg Ile Gly Gly Val Gln Gln Asp Thr Ile 50 55 60
71 50

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73 ctg gcc gag ggc ctt cac ttc agg atc cct tgg ttc cag tac ccc att 422
74 Leu Ala Glu Gly Leu His Phe Arg Ile Pro Trp Phe Gln Tyr Pro Ile
75 65 70 75
77 atc tat gac att cgg gcc aga cct cga aaa atc tcc tcc cct aca ggc 470
78 Ile Tyr Asp Ile Arg Ala Arg Pro Arg Lys Ile Ser Ser Pro Thr Gly
79 80 85 90 95
81 tcc aaa gac cta cag atg gtg aat atc tcc ctg cga gtg ttg tct cga 518
82 Ser Lys Asp Leu Gln Met Val Asn Ile Ser Leu Arg Val Leu Ser Arg
83 100 105 110
85 ccc aat gct cag gag ctt cct agc atg tac cag cgc cta ggg ctg gac 566
86 Pro Asn Ala Gln Glu Leu Pro Ser Met Tyr Gln Arg Leu Gly Leu Asp
87 115 120 125
89 tac gag gaa cga gtg ttg ccg tcc att gtc aac gag gtg ctc aag agt 614
90 Tyr Glu Glu Arg Val Leu Pro Ser Ile Val Asn Glu Val Leu Lys Ser
91 130 135 140
93 gtg gtg gcc aag ttc aat gcc tca cag ctg atc acc cag cgg gcc cag 662
94 Val Val Ala Lys Phe Asn Ala Ser Gln Leu Ile Thr Gln Arg Ala Gln
95 145 150 155
97 gta tcc ctg ttg atc cgc cgg gag ctg aca gag agg gcc aag gac ttc 710
98 Val Ser Leu Leu Ile Arg Arg Glu Leu Thr Glu Arg Ala Lys Asp Phe
99 160 165 170 175
101 agc ctc atc ctg gat gat gtg gcc atc aca gag ctg agc ttt agc cga 758
102 Ser Leu Ile Leu Asp Asp Val Ala Ile Thr Glu Leu Ser Phe Ser Arg
103 180 185 190
105 gag tac aca gct gct gta gaa gcc aaa caa gtg gcc cag cag gag gcc 806
106 Glu Tyr Thr Ala Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu Ala
107 195 200 205
109 cag cgg gcc caa ttc ttg gta gaa aaa gca aag cag gaa cag cgg cag 854
110 Gln Arg Ala Gln Phe Leu Val Glu Lys Ala Lys Gln Glu Gln Arg Gln
111 210 215 220
113 aaa att gtg cag gcc gag ggt gag gcc gag gct gcc aag atg ctt gga 902
114 Lys Ile Val Gln Ala Glu Gly Glu Ala Glu Ala Lys Met Leu Gly
115 225 230 235
117 gaa gca ctg agc aag aac cct ggc tac atc aaa ctt cgc aag att cga 950
118 Glu Ala Leu Ser Lys Asn Pro Gly Tyr Ile Lys Leu Arg Lys Ile Arg
119 240 245 250 255
121 gca gcc cag aat atc tcc aag acg atc gcc aca tca cag aat cgt atc 998
122 Ala Ala Gln Asn Ile Ser Lys Thr Ile Ala Thr Ser Gln Asn Arg Ile
123 260 265 270
125 tat ctc aca gct gac aac ctt gtg ctg aac cta cag gat gaa agt ttc 1046
126 Tyr Leu Thr Ala Asp Asn Leu Val Leu Asn Leu Gln Asp Glu Ser Phe
127 275 280 285
129 acc agg gga agt gac agc ctc atc aag ggt aag aaa tga gcctagtcac 1095
130 Thr Arg Gly Ser Asp Ser Leu Ile Lys Gly Lys Lys
131 290 295
133 caagaactcc acccccagag gaagtggatc tgcttctcca gtttttgagg agccagccag 1155
135 ggggtccagca cagccctacc ccgccccagt atcatgcat ggtccccac accggttccc 1215
137 tgaaccctc ttggattaag gaagactgaa gactagcccc ttttctggga aattactttc 1275
139 ctccctccctg tgttaactgg ggctgttggg gacagtgcgt gatttctcag tgatttcccta 1335

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141 cagtgttggt ccctccctca aggctgggag gagataaaca ccaacccagg aattctcaat 1395
143 aaatTTTTat tacttaacct g 1416
146 <210> SEQ ID NO: 4
147 <211> LENGTH: 21
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
153 <223> OTHER INFORMATION: PCR Primer
155 <400> SEQUENCE: 4 21
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159 <210> SEQ ID NO: 5
160 <211> LENGTH: 20
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
166 <223> OTHER INFORMATION: PCR Primer
168 <400> SEQUENCE: 5 20
169 gtggcgatcg tcttggagat
172 <210> SEQ ID NO: 6
173 <211> LENGTH: 24
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Probe
181 <400> SEQUENCE: 6 24
182 acttcgcaag attcgagcag ccca
185 <210> SEQ ID NO: 7
186 <211> LENGTH: 19
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Primer
194 <400> SEQUENCE: 7 19
195 gaaggtgaag gtcggagtc
198 <210> SEQ ID NO: 8
199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
205 <223> OTHER INFORMATION: PCR Primer
207 <400> SEQUENCE: 8 20
208 gaagatggtg atgggatttc
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR Probe
220 <400> SEQUENCE: 9

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221 caagcttccc gttctcagcc
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 6000
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
231 <221> NAME/KEY: intron
232 <222> LOCATION: (576)...(711)
233 <223> OTHER INFORMATION: intron 1
W--> 235 <221> NAME/KEY: exon:intron junction
236 <222> LOCATION: (796)...(797)
237 <223> OTHER INFORMATION: exon 2:intron 2
W--> 239 <221> NAME/KEY: intron:exon junction
240 <222> LOCATION: (1414)...(1415)
241 <223> OTHER INFORMATION: intron 2:exon 3
W--> 243 <221> NAME/KEY: exon:intron junction
244 <222> LOCATION: (1494)...(1495)
245 <223> OTHER INFORMATION: exon 3:intron 3
247 <221> NAME/KEY: intron
248 <222> LOCATION: (1495)...(2396)
249 <223> OTHER INFORMATION: intron 3
251 <221> NAME/KEY: exon
252 <222> LOCATION: (3213)...(3316)
253 <223> OTHER INFORMATION: exon 6
W--> 255 <221> NAME/KEY: exon:intron junction
256 <222> LOCATION: (3316)...(3317)
257 <223> OTHER INFORMATION: exon 6:intron 6
259 <221> NAME/KEY: intron
260 <222> LOCATION: (3317)...(3743)
261 <223> OTHER INFORMATION: intron 6
W--> 263 <221> NAME/KEY: intron:exon junction
264 <222> LOCATION: (5075)...(5076)
265 <223> OTHER INFORMATION: intron 8:exon 9
267 <400> SEQUENCE: 10
268 tcccagtcct gtgcctgctc cccaccgctt cgttcacgag gcttgaatcc atcactgggc 60
270 gcggccatct tgcaacaata ccggaagttg cgctaacgct cttaaataag aacagcgcg 120
272 cttctaataca caaatttcct tccggctgcc attttgaaag tgggccagga aatggagatg 180
274 acttgctgtc ttgcgtgcc ctccctggga gggcagcctt ccagaaaggg gcgggacttc 240
276 cgtatgcgcg attcctgtgc gcgaagttcg ggtccgtagt gggctaaggg ggagggtttc 300
278 aaagggagcg cacttcgcgt gccctttctt tcgccagcct tacgggcccc aacctcgtg 360
280 tgaaggggtgc agtacctaag ccggagcggg gtagaggcgg gccggcacc cttctgacc 420
282 tccagtgcgc ccggcctcaa gatcagacat ggcccagaac ttgaaggact tggcgggacg 480
284 gctgcccgcg gggccccggg gcatgggcac ggccctgaag ctgttgctgg gggccggcgc 540
286 cgtggcctac ggtgtgcgcg aatctgtgtt caccgggtgag caacctccgc ctgctgcgcg 600
288 gacgcttcca gtccctcccc caaacccctt gccctgtccc cgcgcccctc cacgggccta 660
290 gcatttcctc tgagcagcgg cctggcctga tcaccaccca gtggaaggcg 720
292 ggacacagag catcttcttc aatcggtatg gtggagtgcg gcaggacact atcctggcgc 780
294 agggccttca cttcaggtaa tggcgggcag agcctgctga ccctgacctt tcacccttga 840
296 cgccgaccca gcagtggcta tagtcggacg tgcaacagga ttcaacgctg ctcttttccc 900

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298 accctcctca tccctgcccc taggatagtg ggtgctgcga gaacctccag cagcatacaa 960
300 actgttgttt tocagaggga caagagaatc tctccttgtc tgtggtcgtg gagaggagca 1020
302 ggccaaaaaa cgcgtggtga ggggaaaccg ggcaaggcta gtgaaactgc ggccttttct 1080
304 tttttttttt ttggagaggg agtcttgctc tgctgcccag gctggagtgc agtggcgcgca 1140
306 tctcggtcga ctgcaacctc cgcctcctga tttcaagcga ttctcctgcc tcagcctcac 1200
308 gagtagctgg gattacaggg gcccgccacc acgcccggct aatttttcta ttttagtaga 1260
310 gacgggggtt cactatgtag atcaagctgg tctcgaaact ctgacctcaa atgatccgcc 1320
312 cgcctcggcc tcccaaaagt ctgggattac aggcgtgagc caccgcgcc gcccgaaact 1380
314 gtggcctctt aatacctatc cctgtcctct ccaggatccc ttggttccag taccaccatta 1440
316 tctatgacat tcggggccaga cctcgaaaaa tctcctcccc tacaggctcc aaaggtaggt 1500
318 ctgagcaact ggtaatcaca tggcaggtgg gatgatcaag gtagctggca agaaacccca 1560
320 ggggaatatg gtagtgctcag gccttttaggc ctctttccac atctgcaaga gctgtaacaa 1620
322 aaatacctgc ctccctgggg caaagcagca aattctgaac aactgtgtt tgcgtgcttt 1680
324 ttactgtctc ctccctgacg tgtattcaat aagagtattg tttgtccctc gtcttgttca 1740
326 ctgcctagat caaagctttg ttttaaagcc ttttttttct aactgcttga cttactatat 1800
328 ctacagttac atccactagt acactctgtt ctggagaagt ttgtccctaa gcttgactag 1860
330 ttcacctgtt ctctccttct agaccataca taaaagccgt gcctttgagt tccccagacc 1920
332 tcttctcctt ccccaccac gcacacatat acacctggg tcaggtagct cacctgtaac 1980
334 ctgtaagtga ctctcttctg ctatacctag tgcaggctgc ttattcattt actagactgg 2040
336 gccctgggaa taaaagattc attaaacaca attcttgtcc cccaagtcct tacaggagac 2100
338 atgattacgg tacagcacga aagcgccac gttagaggtt gcacagagta cagaggggga 2160
340 aagagtagtc agctctgctg gtgacgggtt ttgcagttca aggcttcaca gtgggtgagg 2220
342 gtgcatttca gctgtgctgc gtcttgtctt ccttgcagc ctgattaact ctctcccc 2280
344 cagggttagtg ccaggctgta caccattgca cagggcatac agggaggaac atgaaggaga 2340
346 aaatgcttgg gaaaggtgtt ttggccttga ccagccactg ctgacctcaa tctcagacct 2400
348 acagatggtg aatatctccc tgcagtggtt gtctcgaccc aatgctcagg agcttcctag 2460
350 catgtaccag cgcctagggc tggactacga ggaacgagtg ttgccgtcca ttgtcaacga 2520
352 ggtgctcaag agtgtggtgg ccaagttcaa tgcctcacag ctgatcacc agcggggcca 2580
354 ggtctgactc ccaccaccat ctgcgtggtg tcagccttcc cttcctaggg ccagagtatt 2640
356 gggaattagg aaaggcagct tattagaaaa gcattgtcac ctagtgcca tttccacct 2700
358 aaagctgtgc taattgccac tgtgaaataa ggagagccag cattagaact ctagactact 2760
360 cgggtgttag aagcacagag gaaaatggcc aagtcttggc ttttctgca cctcttcgag 2820
362 cagagaggct tatgttacag gtttgccctga caggaagcta aggcagtgc tgttgattg 2880
364 agagtgaagg gttaggggtc gcaaccttcc tttcagctcc ccagtccctt caaaccacc 2940
366 ctcccttccc ctcttcaccc ctgcctcag gtatccctgt tgatccgcc ggagctgaca 3000
368 gagagggcca aggacttcag cctcactctg gatgatgtgg ccatcacaga gctgacttt 3060
370 agccgagagt acacagctgc tgtagaagcc aaacaagtgg gtgagtcgca agagccgtgg 3120
372 ggtgagggct tctgagatgc aggaggagga aagactccat ggggtgggct cctgaccag 3180
374 gacagggctt cctgactct ctccaccac agcccagcag gaggccagc gggcccaatt 3240
376 cttggtagaa aaagcaaagc aggaacagcg gcagaaaatt gtgcaggccg agggtagggc 3300
378 cgaggctgcc aagatgatat ccttctgctg gagagatctc agcccagccc ctagggcacc 3360
380 tgagttcccc attctccttc atgggcaggc tgatgagact aaggcgaatg cgactccgtg 3420
382 ctctctggcc cttggctcct tgttgggggt ggggactaca gatgagatct gaaatcttag 3480
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386 gccttcattt ctggtgctgc ccctagtccc tggcagcagc accttgatc tgacagccca 3600
388 ggggtccacg gtagggctgg gcacaagcca cctgagcgca accttgatc tgacagccca 3660
390 gaggaggact ggagcaaggg agtgtggtaa ggacagggcc agggattgag acctgccctt 3720
392 gcggtgacct taacctcct cacttggag aagcactgag caagaaccct ggctacatca 3780
394 aacttcgcaa gattcgagca gccagaata tctccaagac ggtgagtgtg tcagcccagc 3840

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:235 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:239 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:243 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:255 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10